



SEQUENCE LISTING

<110> STEINMAN, RALPH A
NUSSENZWEIG, MICHEL C
SWIGGARD, WILLIAM J
JIANG, WANPING

<120> IDENTIFICATION OF DEC, A RECEPTOR WITH
C-TYPE LECTIN DOMAINS, NUCLEIC ACIDS ENCODING DEC, AND USES
THEREOF

<130> 600-1-081CON

<140> 09/586,704

<141> 2000-06-05

<150> 08/381,528

<151> 1995-01-31

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 30

<212> PRT

<213> homo sapiens

<220>

<223> C terminal DEC-205

<400> 1

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
			20					25					30		

<210> 2

<211> 25

<212> PRT

<213> homo sapiens

<220>

<223> N terminal DEC-205

<400> 2

Ser	Glu	Ser	Ser	Gly	Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Glu	Asn	Thr
1				5				10					15		
Gly	Lys	Cys	Ile	Gln	Pro	Leu	Phe	Asp							
			20					25							

<210> 3
 <211> 1723
 <212> PRT
 <213> mus musculus

<220>
 <223> predicted DEC-205

<400> 3

Met	Arg	Thr	Gly	Arg	Val	Thr	Pro	Gly	Leu	Ala	Ala	Gly	Leu	Leu	Leu
1				5					10					15	
Leu	Leu	Leu	Arg	Ser	Phe	Gly	Leu	Val	Glu	Pro	Ser	Glu	Ser	Ser	Gly
			20					25					30		
Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Glu	Asn	Thr	Gly	Lys	Cys	Ile	Gln
		35					40					45			
Pro	Leu	Ser	Asp	Trp	Val	Val	Ala	Gln	Asp	Cys	Ser	Gly	Thr	Asn	Asn
	50					55					60				
Met	Leu	Trp	Lys	Trp	Val	Ser	Gln	His	Arg	Leu	Phe	His	Leu	Glu	Ser
65					70					75					80
Gln	Lys	Cys	Leu	Gly	Leu	Asp	Ile	Thr	Lys	Ala	Thr	Asp	Asn	Leu	Arg
				85					90					95	
Met	Phe	Ser	Cys	Asp	Ser	Thr	Val	Met	Leu	Trp	Trp	Lys	Cys	Glu	His
			100					105					110		
His	Ser	Leu	Tyr	Thr	Ala	Ala	Gln	Tyr	Arg	Leu	Ala	Leu	Lys	Asp	Gly
		115					120					125			
Tyr	Ala	Val	Ala	Asn	Thr	Asn	Thr	Ser	Asp	Val	Trp	Lys	Lys	Gly	Gly
	130					135					140				
Ser	Glu	Glu	Asn	Leu	Cys	Ala	Gln	Pro	Tyr	His	Glu	Ile	Tyr	Thr	Arg
145					150					155					160
Asp	Gly	Asn	Ser	Tyr	Gly	Arg	Pro	Cys	Glu	Phe	Pro	Phe	Leu	Ile	Gly
				165					170					175	
Glu	Thr	Trp	Tyr	His	Asp	Cys	Ile	His	Asp	Glu	Asp	His	Ser	Gly	Pro
		180						185					190		
Trp	Cys	Ala	Thr	Thr	Leu	Ser	Tyr	Glu	Tyr	Asp	Gln	Lys	Trp	Gly	Ile
		195					200					205			
Cys	Leu	Leu	Pro	Glu	Ser	Gly	Cys	Glu	Gly	Asn	Trp	Glu	Lys	Asn	Glu
	210					215					220				
Gln	Ile	Gly	Ser	Cys	Tyr	Gln	Phe	Asn	Asn	Gln	Glu	Ile	Leu	Ser	Trp
225					230					235					240
Lys	Glu	Ala	Tyr	Val	Ser	Cys	Gln	Asn	Gln	Gly	Ala	Asp	Leu	Leu	Ser
				245					250					255	
Ile	His	Ser	Ala	Ala	Glu	Leu	Ala	Tyr	Ile	Thr	Gly	Lys	Glu	Asp	Ile
			260					265					270		
Ala	Arg	Leu	Val	Trp	Leu	Gly	Leu	Asn	Gln	Leu	Tyr	Ser	Ala	Arg	Gly
		275					280					285			
Trp	Glu	Trp	Ser	Asp	Phe	Arg	Pro	Leu	Lys	Phe	Leu	Asn	Trp	Asp	Pro
	290					295					300				
Gly	Thr	Pro	Val	Ala	Pro	Val	Ile	Gly	Gly	Ser	Ser	Cys	Ala	Arg	Met
305					310					315					320
Asp	Thr	Glu	Ser	Gly	Leu	Trp	Gln	Ser	Val	Ser	Cys	Glu	Ser	Gln	Gln
				325					330					335	
Pro	Tyr	Val	Cys	Lys	Lys	Pro	Leu	Asn	Thr	Leu	Glu	Leu	Pro	Asp	
			340					345				350			
Val	Trp	Thr	Tyr	Thr	Asp	Thr	His	Cys	His	Val	Gly	Trp	Leu	Pro	Asn
		355					360					365			
Asn	Gly	Phe	Cys	Tyr	Leu	Leu	Ala	Asn	Glu	Ser	Ser	Ser	Trp	Asp	Ala
	370						375								

Ala	His	Leu	Lys	Cys	Lys	Ala	Phe	Gly	Ala	Asp	Leu	Ile	Ser	Met	His
385					390					395					400
Ser	Leu	Ala	Asp	Val	Glu	Val	Val	Val	Thr	Lys	Leu	His	Asn	Gly	Asp
				405					410					415	
Val	Lys	Lys	Glu	Ile	Trp	Thr	Gly	Leu	Lys	Asn	Thr	Asn	Ser	Pro	Ala
			420					425					430		
Leu	Phe	Gln	Trp	Ser	Asp	Gly	Thr	Glu	Val	Thr	Leu	Thr	Tyr	Trp	Asn
		435					440					445			
Glu	Asn	Glu	Pro	Ser	Val	Pro	Phe	Asn	Lys	Thr	Pro	Asn	Cys	Val	Ser
	450					455					460				
Tyr	Leu	Gly	Lys	Leu	Gly	Gln	Trp	Lys	Val	Gln	Ser	Cys	Glu	Lys	Lys
465					470					475					480
Leu	Arg	Tyr	Val	Cys	Lys	Lys	Lys	Gly	Glu	Ile	Thr	Lys	Asp	Ala	Glu
				485					490					495	
Ser	Asp	Lys	Leu	Cys	Pro	Pro	Asp	Glu	Gly	Trp	Lys	Arg	His	Gly	Glu
			500					505					510		
Thr	Cys	Tyr	Lys	Ile	Tyr	Glu	Lys	Glu	Ala	Pro	Phe	Gly	Thr	Asn	Cys
		515					520					525			
Asn	Leu	Thr	Ile	Thr	Ser	Arg	Phe	Glu	Gln	Glu	Phe	Leu	Asn	Tyr	Met
	530					535					540				
Met	Lys	Asn	Tyr	Asp	Lys	Ser	Leu	Arg	Lys	Tyr	Phe	Trp	Thr	Gly	Leu
545					550					555					560
Arg	Asp	Pro	Asp	Ser	Arg	Gly	Glu	Tyr	Ser	Trp	Ala	Val	Ala	Gln	Gly
				565					570					575	
Val	Lys	Gln	Ala	Val	Thr	Phe	Ser	Asn	Trp	Asn	Phe	Leu	Glu	Pro	Ala
			580					585				590			
Ser	Pro	Gly	Gly	Cys	Val	Ala	Met	Ser	Thr	Gly	Lys	Thr	Leu	Gly	Lys
		595					600					605			
Trp	Glu	Val	Lys	Asn	Cys	Arg	Ser	Phe	Arg	Ala	Leu	Ser	Ile	Cys	Lys
	610					615					620				
Lys	Val	Ser	Glu	Pro	Gln	Glu	Pro	Glu	Glu	Ala	Ala	Pro	Lys	Pro	Asp
625					630					635					640
Asp	Pro	Cys	Pro	Glu	Gly	Trp	His	Thr	Phe	Pro	Ser	Ser	Leu	Ser	Cys
				645					650					655	
Tyr	Lys	Val	Phe	His	Ile	Glu	Arg	Ile	Val	Arg	Lys	Arg	Asn	Trp	Glu
			660					665					670		
Glu	Ala	Glu	Arg	Phe	Cys	Gln	Ala	Leu	Gly	Ala	His	Leu	Pro	Ser	Phe
		675					680					685			
Ser	Arg	Arg	Glu	Glu	Ile	Lys	Asp	Phe	Val	His	Leu	Leu	Lys	Asp	Gln
	690					695					700				
Phe	Ser	Gly	Gln	Arg	Trp	Leu	Trp	Ile	Gly	Leu	Asn	Lys	Arg	Ser	Pro
705					710					715					720
Asp	Leu	Gln	Gly	Ser	Trp	Gln	Trp	Ser	Asp	Arg	Thr	Pro	Val	Ser	Ala
				725					730					735	
Val	Met	Met	Glu	Pro	Glu	Phe	Gln	Gln	Asp	Phe	Asp	Ile	Arg	Asp	Cys
			740					745					750		
Ala	Ala	Ile	Lys	Val	Leu	Asp	Val	Pro	Trp	Arg	Arg	Val	Trp	His	Leu
		755					760					765			
Tyr	Glu	Asp	Lys	Asp	Tyr	Ala	Tyr	Trp	Lys	Pro	Phe	Ala	Cys	Asp	Ala
770					775						780				
Lys	Leu	Glu	Trp	Val	Cys	Gln	Ile	Pro	Lys	Gly	Ser	Thr	Pro	Gln	Met
785					790					795					800
Pro	Asp	Trp	Tyr	Asn	Pro	Glu	Arg	Thr	Gly	Ile	His	Gly	Pro	Pro	Val
				805					810					815	
Ile	Ile	Glu	Gly	Ser	Glu	Tyr	Trp	Phe	Val	Ala	Asp	Pro	His	Leu	Asn
			820					825					830		
Tyr	Glu	Glu	Ala	Val	Leu	Tyr	Cys	Ala	Ser	Asn	His	Ser	Phe	Leu	Ala

835	840	845
Thr Ile Thr Ser Phe Thr Gly Leu Lys Ala Ile Lys Asn Lys Leu Ala		
850	855	860
Asn Ile Ser Gly Glu Glu Gln Lys Trp Trp Val Lys Thr Ser Glu Asn		
865	870	875
Pro Ile Asp Arg Tyr Phe Leu Gly Ser Arg Arg Arg Leu Trp His His		
885	890	895
Phe Pro Met Thr Phe Gly Asp Glu Cys Leu His Met Ser Ala Lys Thr		
900	905	910
Trp Leu Val Asp Leu Ser Lys Arg Ala Asp Cys Asn Ala Lys Leu Pro		
915	920	925
Phe Ile Cys Glu Arg Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro		
930	935	940
Asp Pro Ala Ala Lys Val Gln Cys Thr Glu Lys Trp Ile Pro Phe Gln		
945	950	955
Asn Lys Cys Phe Leu Lys Val Asn Ser Gly Pro Val Thr Phe Ser Gln		
965	970	975
Ala Ser Gly Ile Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu		
980	985	990
Ser Arg Gly Glu Gln Asp Phe Ile Ile Ser Leu Leu Pro Glu Met Glu		
995	1000	1005
Ala Ser Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Arg Ile Asn		
1010	1015	1020
Arg Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro Leu		
1025	1030	1035
Leu Val Gly Arg Arg Leu Ser Ile Pro Thr Asn Phe Phe Asp Asp Glu		
1045	1050	1055
Ser His Phe His Cys Ala Leu Ile Leu Asn Leu Lys Lys Ser Pro Leu		
1060	1065	1070
Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg His Ser Leu Ser		
1075	1080	1085
Leu Cys Gln Lys Tyr Ser Glu Thr Glu Asp Gly Gln Pro Trp Glu Asn		
1090	1095	1100
Thr Ser Lys Thr Val Lys Tyr Leu Asn Asn Leu Tyr Lys Ile Ile Ser		
1105	1110	1115
Lys Pro Leu Thr Trp His Gly Ala Leu Lys Glu Cys Met Lys Glu Lys		
1125	1130	1135
Met Arg Leu Val Ser Ile Thr Asp Pro Tyr Gln Gln Ala Phe Leu Ala		
1140	1145	1150
Val Gln Ala Thr Leu Arg Asn Ser Ser Phe Trp Ile Gly Leu Ser Ser		
1155	1160	1165
Gln Asp Asp Glu Leu Asn Phe Gly Trp Ser Asp Gly Lys Arg Leu Gln		
1170	1175	1180
Phe Ser Asn Trp Ala Gly Ser Asn Glu Gln Leu Asp Asp Cys Val Ile		
1185	1190	1195
Leu Asp Thr Asp Gly Phe Trp Lys Thr Ala Asp Cys Asp Asp Asn Gln		
1205	1210	1215
Pro Gly Ala Ile Cys Tyr Tyr Pro Gly Asn Glu Thr Glu Glu Glu Val		
1220	1225	1230
Arg Ala Leu Asp Thr Ala Lys Cys Pro Ser Pro Val Gln Ser Thr Pro		
1235	1240	1245
Trp Ile Pro Phe Gln Asn Ser Cys Tyr Asn Phe Met Ile Thr Asn Asn		
1250	1255	1260
Arg His Lys Thr Val Thr Pro Glu Glu Val Gln Ser Thr Cys Glu Lys		
1265	1270	1275
Leu His Pro Lys Ala His Ser Leu Ser Ile Arg Asn Glu Glu Glu Asn		
1285	1290	1295

Thr	Phe	Val	Val	Glu	Gln	Leu	Leu	Tyr	Phe	Asn	Tyr	Ile	Ala	Ser	Trp	
			1300					1305					1310			
Val	Met	Leu	Gly	Ile	Thr	Tyr	Glu	Asn	Asn	Ser	Leu	Met	Trp	Phe	Asp	
		1315					1320					1325				
Lys	Thr	Ala	Leu	Ser	Tyr	Thr	His	Trp	Arg	Thr	Gly	Arg	Pro	Thr	Val	
	1330					1335					1340					
Lys	Asn	Gly	Lys	Phe	Leu	Ala	Gly	Leu	Ser	Thr	Asp	Gly	Phe	Trp	Asp	
1345					1350					1355					1360	
Ile	Gln	Ser	Phe	Asn	Val	Ile	Glu	Glu	Thr	Leu	His	Phe	Tyr	Gln	His	
				1365					1370					1375		
Ser	Ile	Ser	Ala	Cys	Lys	Ile	Glu	Met	Val	Asp	Tyr	Glu	Asp	Lys	His	
			1380					1385					1390			
Asn	Gly	Thr	Leu	Pro	Gln	Phe	Ile	Pro	Tyr	Lys	Asp	Gly	Val	Tyr	Ser	
	1395							1400					1405			
Val	Ile	Gln	Lys	Lys	Val	Thr	Trp	Tyr	Glu	Ala	Leu	Asn	Ala	Cys	Ser	
	1410					1415						1420				
Gln	Ser	Gly	Gly	Glu	Leu	Ala	Ser	Val	His	Asn	Pro	Asn	Gly	Lys	Leu	
1425					1430					1435					1440	
Phe	Leu	Glu	Asp	Ile	Val	Asn	Arg	Asp	Gly	Phe	Pro	Leu	Trp	Val	Gly	
				1445					1450					1455		
Leu	Ser	Ser	His	Asp	Gly	Ser	Glu	Ser	Ser	Phe	Glu	Trp	Ser	Asp	Gly	
			1460					1465					1470			
Arg	Ala	Phe	Asp	Tyr	Val	Pro	Trp	Gln	Ser	Leu	Gln	Ser	Pro	Gly	Asp	
	1475						1480					1485				
Cys	Val	Val	Leu	Tyr	Pro	Lys	Gly	Ile	Trp	Arg	Arg	Glu	Lys	Cys	Leu	
	1490					1495					1500					
Ser	Val	Lys	Asp	Gly	Ala	Ile	Cys	Tyr	Lys	Pro	Thr	Lys	Asp	Lys	Lys	
1505					1510					1515					1520	
Leu	Ile	Phe	His	Val	Lys	Ser	Ser	Lys	Cys	Pro	Val	Ala	Lys	Arg	Asp	
				1525					1530					1535		
Gly	Pro	Gln	Trp	Val	Gln	Tyr	Gly	Gly	His	Cys	Tyr	Ala	Ser	Asp	Gln	
	1540						1545						1550			
Val	Leu	His	Ser	Phe	Ser	Glu	Ala	Lys	Gln	Val	Cys	Gln	Glu	Leu	Asp	
	1555						1560					1565				
His	Ser	Ala	Thr	Val	Val	Thr	Ile	Ala	Asp	Glu	Asn	Glu	Asn	Lys	Phe	
	1570					1575					1580					
Val	Ser	Arg	Leu	Met	Arg	Glu	Asn	Tyr	Asn	Ile	Thr	Met	Arg	Val	Trp	
1585					1590					1595					1600	
Leu	Gly	Leu	Ser	Gln	His	Ser	Leu	Asp	Gln	Ser	Trp	Ser	Trp	Leu	Asp	
				1605					1610					1615		
Gly	Leu	Asp	Val	Thr	Phe	Val	Lys	Trp	Glu	Asn	Lys	Thr	Lys	Asp	Gly	
	1620							1625					1630			
Asp	Gly	Lys	Cys	Ser	Ile	Leu	Ile	Ala	Ser	Asn	Glu	Thr	Trp	Arg	Lys	
	1635					1640					1645					
Val	His	Cys	Ser	Arg	Gly	Tyr	Ala	Arg	Ala	Val	Cys	Lys	Ile	Pro	Leu	
	1650					1655					1660					
Ser	Pro	Asp	Tyr	Thr	Gly	Ile	Ala	Ile	Leu	Phe	Ala	Val	Leu	Cys	Leu	
1665					1670					1675					1680	
Leu	Gly	Leu	Ile	Ser	Leu	Ala	Ile	Trp	Phe	Leu	Leu	Gln	Arg	Ser	His	
				1685					1690					1695		
Ile	Arg	Trp	Thr	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Glu	His	Gly	Thr	Asn	
	1700							1705					1710			
Glu	Asp	Glu	Val	Met	Leu	Pro	Ser	Phe	His	Asp						
	1715						1720									

<211> 1462
 <212> PRT
 <213> bos taurus

<220>
 <223> PLA2 receptor

<400> 4

Met	Pro	Leu	Leu	Ser	Leu	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Val	Pro
1				5					10					15	
Ala	Gly	Ser	Ala	Glu	Thr	Ala	Ala	Trp	Ala	Val	Thr	Pro	Glu	Arg	Leu
			20					25					30		
Arg	Glu	Trp	Gln	Asp	Lys	Gly	Ile	Phe	Ile	Ile	Gln	Ser	Glu	Asn	Leu
		35					40					45			
Glu	Lys	Cys	Ile	Gln	Ala	Ser	Lys	Ser	Thr	Leu	Thr	Leu	Glu	Asn	Cys
	50					55					60				
Lys	Pro	Pro	Asn	Lys	Tyr	Met	Leu	Trp	Lys	Trp	Val	Ser	Asn	His	Arg
65					70					75					80
Leu	Phe	Asn	Ile	Gly	Gly	Ser	Gly	Cys	Leu	Gly	Leu	Asn	Val	Ser	Ser
				85					90					95	
Pro	Glu	Gln	Pro	Leu	Ser	Ile	Tyr	Glu	Cys	Asp	Ser	Thr	His	Val	Ser
			100					105					110		
Leu	Lys	Trp	His	Cys	Asn	Lys	Lys	Thr	Ile	Thr	Gly	Pro	Leu	Gln	Tyr
		115					120					125			
Leu	Val	Gln	Val	Lys	Gln	Asp	Asn	Thr	Leu	Val	Ala	Ser	Arg	Lys	Tyr
						135					140				
Leu	His	Lys	Trp	Val	Ser	Tyr	Met	Ser	Gly	Gly	Gly	Gly	Ile	Cys	Asp
145					150					155					160
Tyr	Leu	His	Lys	Asp	Leu	Tyr	Thr	Ile	Lys	Gly	Asn	Ala	His	Gly	Thr
				165					170					175	
Pro	Cys	Met	Phe	Pro	Phe	Gln	Tyr	Asn	Gln	Gln	Trp	His	His	Glu	Cys
			180					185					190		
Thr	Arg	Glu	Gly	Arg	Glu	Asp	Asn	Leu	Leu	Trp	Cys	Ala	Thr	Thr	Ser
		195					200					205			
Arg	Tyr	Glu	Arg	Asp	Glu	Lys	Trp	Gly	Phe	Cys	Pro	Asp	Pro	Thr	Ser
	210					215					220				
Thr	Glu	Val	Gly	Cys	Asp	Ala	Val	Trp	Glu	Lys	Asp	Leu	His	Ser	Arg
225					230					235					240
Ile	Cys	Tyr	Gln	Phe	Asn	Leu	Leu	Ser	Ser	Leu	Ser	Trp	Ser	Glu	Ala
				245					250					255	
His	Ser	Ser	Cys	Gln	Met	Gln	Gly	Ala	Ala	Leu	Leu	Ser	Ile	Ala	Asp
			260					265					270		
Glu	Thr	Glu	Glu	Asn	Phe	Val	Arg	Lys	His	Leu	Gly	Ser	Glu	Ala	Val
		275					280					285			
Glu	Val	Trp	Met	Gly	Leu	Asn	Gln	Leu	Asp	Glu	Asp	Ala	Gly	Trp	Gln
	290					295					300				
Trp	Ser	Asp	Arg	Thr	Pro	Leu	Asn	Tyr	Leu	Asn	Trp	Lys	Pro	Glu	Ile
305					310					315					320
Asn	Phe	Glu	Pro	Phe	Val	Glu	Tyr	His	Cys	Gly	Thr	Phe	Asn	Ala	Phe
				325					330					335	
Met	Pro	Lys	Ala	Trp	Lys	Ser	Arg	Asp	Cys	Glu	Ser	Thr	Leu	Pro	Tyr
			340					345					350		
Val	Cys	Lys	Lys	Tyr	Leu	Asn	Pro	Thr	Asp	His	Gly	Val	Val	Glu	Lys
		355					360					365			
Asp	Ala	Trp	Lys	Tyr	Tyr	Ala	Thr	His	Cys	Glu	Pro	Gly	Trp	Asn	Pro
	370					375					380				
His	Asn	Arg	Asn	Cys	Tyr	Lys	Leu	Gln	Lys	Glu	Lys	Lys	Thr	Trp	Asn

385					390					395					400
Glu	Ala	Leu	Gln	Ser	Cys	Gln	Ser	Asn	Asn	Ser	Val	Leu	Thr	Asp	Ile
				405					410					415	
Thr	Ser	Leu	Ala	Glu	Val	Glu	Phe	Leu	Val	Thr	Leu	Leu	Gly	Asp	Glu
			420					425					430		
Asn	Ala	Ser	Glu	Thr	Trp	Ile	Gly	Leu	Ser	Ser	His	Lys	Ile	Pro	Val
		435					440					445			
Ser	Phe	Glu	Trp	Ser	Asn	Gly	Ser	Ser	Val	Thr	Phe	Thr	Asn	Trp	His
	450					455					460				
Thr	Leu	Glu	Pro	His	Ile	Phe	Pro	Asn	Arg	Ser	Gln	Leu	Cys	Val	Ser
465					470					475					480
Ala	Glu	Gln	Ser	Glu	Gly	His	Trp	Lys	Val	Lys	Asn	Cys	Glu	Glu	Thr
				485					490					495	
Leu	Phe	Tyr	Leu	Cys	Lys	Lys	Thr	His	Leu	Val	Leu	Ser	Asp	Thr	Glu
			500					505					510		
Ser	Gly	Cys	Gln	Lys	Gly	Trp	Glu	Arg	His	Gly	Lys	Phe	Cys	Tyr	Lys
		515					520					525			
Ile	Asp	Thr	Val	Leu	Arg	Ser	Phe	Asp	His	Ala	Ser	Ser	Gly	Tyr	Tyr
	530					535					540				
Cys	Pro	Pro	Ala	Leu	Ile	Thr	Ile	Thr	Ser	Arg	Phe	Glu	Gln	Ala	Phe
545					550					555					560
Ile	Thr	Ser	Leu	Ile	Ser	Ser	Val	Val	Lys	Thr	Lys	Asp	Thr	Tyr	Phe
				565					570					575	
Trp	Ile	Ala	Leu	Gln	Asp	Gln	Asn	Asn	Thr	Gly	Glu	Tyr	Thr	Trp	Lys
			580					585					590		
Thr	Ala	Gly	Gln	Gln	Leu	Glu	Pro	Val	Lys	Tyr	Thr	His	Trp	Asn	Thr
		595					600					605			
Arg	Gln	Pro	Arg	Tyr	Ser	Gly	Gly	Cys	Val	Val	Met	Arg	Gly	Arg	Ser
	610					615					620				
His	Pro	Gly	Arg	Trp	Glu	Val	Arg	Asp	Cys	Arg	His	Phe	Lys	Ala	Met
625					630					635					640
Ser	Leu	Cys	Lys	Gln	Pro	Val	Glu	Asn	Arg	Glu	Lys	Thr	Lys	Gln	Glu
				645					650					655	
Glu	Gly	Trp	Pro	Phe	His	Pro	Cys	Tyr	Leu	Asp	Trp	Glu	Ser	Glu	Pro
			660					665					670		
Gly	Leu	Ala	Ser	Cys	Phe	Lys	Val	Phe	His	Ser	Glu	Lys	Val	Leu	Met
		675					680					685			
Lys	Arg	Thr	Trp	Arg	Gln	Ala	Glu	Glu	Phe	Cys	Glu	Glu	Phe	Gly	Ala
	690					695					700				
His	Leu	Ala	Ser	Phe	Ala	His	Ile	Glu	Glu	Glu	Asn	Phe	Val	Asn	Glu
705					710					715					720
Leu	Leu	His	Ser	Lys	Phe	Asn	Arg	Thr	Glu	Glu	Arg	Gln	Phe	Trp	Ile
				725					730					735	
Gly	Phe	Asn	Lys	Arg	Asn	Pro	Leu	Asn	Ala	Gly	Ser	Trp	Glu	Trp	Ser
			740					745					750		
Asp	Gly	Thr	Pro	Val	Val	Ser	Ser	Phe	Leu	Asp	Asn	Ser	Tyr	Phe	Gly
	755						760					765			
Glu	Asp	Ala	Arg	Asn	Cys	Ala	Val	Tyr	Lys	Ala	Asn	Lys	Thr	Leu	Leu
	770					775					780				
Pro	Ser	Tyr	Cys	Gly	Ser	Lys	Arg	Glu	Trp	Ile	Cys	Lys	Ile	Pro	Arg
785					790					795					800
Asp	Val	Arg	Pro	Lys	Val	Pro	Pro	Trp	Tyr	Gln	Tyr	Asp	Ala	Pro	Trp
				805					810					815	
Leu	Phe	Tyr	Gln	Asp	Ala	Glu	Tyr	Leu	Phe	His	Ile	Ser	Ala	Ser	Glu
			820					825					830		
Trp	Ser	Ser	Phe	Glu	Phe	Val	Cys	Gly	Trp	Leu	Arg	Ser	Asp	Ile	Leu
		835					840					845			

Thr	Ile	His	Ser	Ala	His	Glu	Gln	Glu	Phe	Ile	His	Ser	Lys	Ile	Arg
850						855					860				
Ala	Leu	Ser	Lys	Tyr	Gly	Val	Asn	Trp	Trp	Ile	Gly	Leu	Arg	Glu	Glu
865					870					875					880
Arg	Ala	Ser	Asp	Glu	Phe	Arg	Trp	Arg	Asp	Gly	Ser	Pro	Val	Ile	Tyr
				885					890					895	
Gln	Asn	Trp	Asp	Lys	Gly	Lys	Glu	Arg	Ser	Met	Gly	Leu	Asn	Glu	Ser
			900					905					910		
Gln	Arg	Cys	Gly	Phe	Ile	Ser	Ser	Ile	Thr	Gly	Leu	Trp	Ala	Ser	Glu
			915				920					925			
Glu	Cys	Ser	Ile	Ser	Met	Pro	Ser	Ile	Cys	Lys	Arg	Lys	Lys	Val	Trp
	930					935					940				
Val	Ile	Glu	Lys	Lys	Lys	Asp	Ile	Pro	Lys	Gln	His	Gly	Thr	Cys	Pro
945					950					955					960
Lys	Gly	Trp	Leu	Tyr	Phe	Asp	Tyr	Lys	Cys	Leu	Leu	Leu	Lys	Ile	Pro
				965					970					975	
Glu	Gly	Pro	Ser	Asp	Trp	Lys	Asn	Trp	Thr	Ser	Ala	Gln	Asp	Phe	Cys
			980					985					990		
Val	Glu	Glu	Gly	Gly	Thr	Leu	Val	Ala	Ile	Glu	Asn	Glu	Val	Glu	Gln
			995				1000					1005			
Ala	Phe	Ile	Thr	Met	Asn	Leu	Phe	Gly	His	Thr	Thr	Asn	Val	Trp	Ile
	1010					1015					1020				
Gly	Leu	Gln	Asp	Asp	Asp	Tyr	Glu	Lys	Trp	Leu	Asn	Gly	Arg	Pro	Val
1025					1030					1035					1040
Ser	Tyr	Ser	Asn	Trp	Ser	Pro	Phe	Asp	Thr	Lys	Asn	Ile	Pro	Asn	His
			1045						1050					1055	
Asn	Thr	Thr	Glu	Val	Gln	Lys	Arg	Ile	Pro	Leu	Cys	Gly	Leu	Leu	Ser
			1060					1065					1070		
Asn	Asn	Pro	Asn	Phe	His	Phe	Thr	Gly	Lys	Trp	Tyr	Phe	Asp	Cys	Arg
		1075					1080					1085			
Glu	Gly	Tyr	Gly	Phe	Val	Cys	Glu	Lys	Met	Gln	Asp	Ala	Ser	Gly	His
	1090					1095				1100					
Ser	Ile	Asn	Thr	Ser	Asp	Met	Tyr	Pro	Ile	Pro	Asn	Thr	Leu	Glu	Tyr
1105					1110					1115					1120
Gly	Asn	Arg	Thr	Tyr	Lys	Ile	Ile	Asn	Ala	Asn	Met	Thr	Trp	Tyr	Thr
			1125						1130					1135	
Ala	Leu	Lys	Thr	Cys	Leu	Met	His	Gly	Ala	Glu	Leu	Ala	Ser	Ile	Thr
			1140					1145					1150		
Asp	Gln	Tyr	His	Gln	Ser	Phe	Leu	Thr	Val	Ile	Leu	Asn	Arg	Val	Gly
	1155						1160					1165			
Tyr	Ala	His	Trp	Ile	Gly	Leu	Phe	Thr	Glu	Asp	Asn	Gly	Leu	Ser	Phe
	1170					1175				1180					
Asp	Trp	Ser	Asp	Gly	Thr	Lys	Ser	Ser	Phe	Thr	Phe	Trp	Lys	Asp	Asp
1185				1190						1195					

		195					200					205						
Cys	Pro	Leu	Lys	Phe	Glu	Gly	Ser	Glu	Ser	Leu	Trp	Asn	Lys	Asp	Pro			
	210					215					220							
Leu	Thr	Ser	Val	Ser	Tyr	Gln	Ile	Asn	Ser	Lys	Ser	Ala	Leu	Thr	Trp			
225					230					235					240			
His	Gln	Ala	Arg	Lys	Ser	Cys	Gln	Gln	Gln	Asn	Ala	Glu	Leu	Leu	Ser			
				245						250					255			
Ile	Thr	Glu	Ile	His	Glu	Gln	Thr	Tyr	Leu	Thr	Gly	Leu	Thr	Ser	Ser			
			260					265						270				
Leu	Thr	Ser	Gly	Leu	Trp	Ile	Gly	Leu	Asn	Ser	Leu	Ser	Phe	Asn	Ser			
		275					280					285						
Gly	Trp	Gln	Trp	Ser	Asp	Arg	Ser	Pro	Phe	Arg	Tyr	Leu	Asn	Trp	Leu			
	290					295					300							
Pro	Gly	Ser	Pro	Ser	Ala	Glu	Pro	Gly	Lys	Ser	Cys	Val	Ser	Leu	Asn			
305					310						315				320			
Pro	Gly	Lys	Asn	Ala	Lys	Trp	Glu	Asn	Leu	Glu	Cys	Val	Gln	Lys	Leu			
				325							330				335			
Gly	Tyr	Ile	Cys	Lys	Lys	Gly	Asn	Thr	Thr	Leu	Asn	Ser	Phe	Val	Ile			
			340					345						350				
Pro	Ser	Glu	Ser	Asp	Val	Pro	Thr	His	Cys	Pro	Ser	Gln	Trp	Trp	Pro			
		355					360					365						
Tyr	Ala	Gly	His	Cys	Tyr	Lys	Ile	His	Arg	Asp	Glu	Lys	Lys	Ile	Gln			
	370					375					380							
Arg	Asp	Ala	Leu	Thr	Thr	Cys	Arg	Lys	Glu	Gly	Gly	Asp	Leu	Thr	Ser			
385					390					395					400			
Ile	His	Thr	Ile	Glu	Glu	Leu	Asp	Phe	Ile	Ile	Ser	Gln	Leu	Gly	Tyr			
				405					410					415				
Glu	Pro	Asn	Asp	Glu	Leu	Trp	Ile	Gly	Leu	Asn	Asp	Ile	Lys	Ile	Gln			
			420					425					430					
Met	Tyr	Phe	Glu	Trp	Ser	Asp	Gly	Thr	Pro	Val	Thr	Phe	Thr	Lys	Trp			
		435					440					445						
Leu	Arg	Gly	Glu	Pro	Ser	His	Glu	Asn	Asn	Arg	Gln	Glu	Asp	Cys	Val			
	450					455					460							
Val	Met	Lys	Gly	Lys	Asp	Gly	Tyr	Trp	Ala	Asp	Arg	Gly	Cys	Glu	Trp			
465					470					475					480			
Pro	Leu	Gly	Tyr	Ile	Cys	Lys	Met	Lys	Ser	Arg	Ser	Gln	Gly	Pro	Glu			
				485					490					495				
Ile	Val	Glu	Val	Glu	Lys	Gly	Cys	Arg	Lys	Gly	Trp	Lys	Lys	His	His			
			500					505						510				
Phe	Tyr	Cys	Tyr	Met	Ile	Gly	His	Thr	Leu	Ser	Thr	Phe	Ala	Glu	Ala			
		515					520					525						
Asn	Gln	Thr	Cys	Asn	Asn	Glu	Asn	Ala	Tyr	Leu	Thr	Thr	Ile	Glu	Asp			
	530					535					540							

Ser	Leu	Cys	Phe	Lys	Leu	Tyr	Ala	Lys	Gly	Lys	His	Glu	Lys	Lys	Thr	660	665	670
Trp	Phe	Glu	Ser	Arg	Asp	Phe	Cys	Arg	Ala	Leu	Gly	Gly	Asp	Leu	Ala	675	680	685
Ser	Ile	Asn	Asn	Lys	Glu	Glu	Gln	Gln	Thr	Ile	Trp	Arg	Leu	Ile	Thr	690	695	700
Ala	Ser	Gly	Ser	Tyr	His	Lys	Leu	Phe	Trp	Leu	Gly	Leu	Thr	Tyr	Gly	705	710	715
Ser	Pro	Ser	Glu	Gly	Phe	Thr	Trp	Ser	Asp	Gly	Ser	Pro	Val	Ser	Tyr	725	730	735
Glu	Asn	Trp	Ala	Tyr	Gly	Glu	Pro	Asn	Asn	Tyr	Gln	Asn	Val	Glu	Tyr	740	745	750
Cys	Gly	Glu	Leu	Lys	Gly	Asp	Pro	Thr	Met	Ser	Trp	Asn	Asp	Ile	Asn	755	760	765
Cys	Glu	His	Leu	Asn	Asn	Trp	Ile	Cys	Gln	Ile	Gln	Lys	Gly	Gln	Thr	770	775	780
Pro	Lys	Pro	Glu	Pro	Thr	Pro	Ala	Pro	Gln	Asp	Asn	Pro	Pro	Val	Thr	785	790	795
Glu	Asp	Gly	Trp	Val	Ile	Tyr	Lys	Asp	Tyr	Gln	Tyr	Tyr	Phe	Ser	Lys	805	810	815
Glu	Lys	Glu	Thr	Met	Asp	Asn	Ala	Arg	Ala	Phe	Cys	Lys	Arg	Asn	Phe	820	825	830
Gly	Asp	Leu	Val	Ser	Ile	Gln	Ser	Glu	Ser	Glu	Lys	Lys	Phe	Leu	Trp	835	840	845
Lys	Tyr	Val	Asn	Arg	Asn	Asp	Ala	Gln	Ser	Ala	Tyr	Phe	Ile	Gly	Leu	850	855	860
Leu	Ile	Ser	Leu	Asp	Lys	Lys	Phe	Ala	Trp	Met	Asp	Gly	Ser	Lys	Val	865	870	875
Asp	Tyr	Val	Ser	Trp	Ala	Thr	Gly	Glu	Pro	Asn	Phe	Ala	Asn	Glu	Asp	885	890	895
Glu	Asn	Cys	Val	Thr	Met	Tyr	Ser	Asn	Ser	Gly	Phe	Trp	Asn	Asp	Ile	900	905	910
Asn	Cys	Gly	Tyr	Pro	Asn	Ala	Phe	Ile	Cys	Gln	Arg	His	Asn	Ser	Ser	915	920	925
Ile	Asn	Ala	Thr	Thr	Val	Met	Pro	Thr	Met	Pro	Ser	Val	Pro	Ser	Gly	930	935	940
Cys	Lys	Glu	Gly	Trp	Asn	Phe	Tyr	Ser	Asn	Lys	Cys	Phe	Lys	Ile	Phe	945	950	955
Gly	Phe	Met	Glu	Glu	Glu	Arg	Lys	Asn	Trp	Gln	Glu	Ala	Arg	Lys	Ala	965	970	975
Cys	Ile	Gly	Phe	Gly	Gly	Asn	Leu	Val	Ser	Ile	Gln	Asn	Glu	Lys	Glu	980	985	990
Gln	Ala	Phe	Leu	Thr	Tyr	His	Met	Lys	Asp	Ser	Thr	Phe	Ser	Ala	Trp	995	1000	1005
Thr	Gly	Leu	Asn	Asp	Val	Asn	Ser	Glu	His	Thr	Phe	Leu	Trp	Thr	Asp	1010	1015	1020
Gly	Arg	Gly	Val	His	Tyr	Thr	Asn	Trp	Gly	Lys	Gly	Tyr	Pro	Gly	Gly	1025	1030	1035
Arg	Arg	Ser	Ser	Leu	Ser	Tyr	Glu	Asp	Ala	Asp	Cys	Val	Val	Ile	Ile	1045	1050	1055
Gly	Gly	Ala	Ser	Asn	Glu	Ala	Gly	Lys	Trp	Met	Asp	Asp	Thr	Cys	Asp	1060	1065	1070
Ser	Lys	Arg	Gly	Tyr	Ile	Cys	Gln	Thr	Arg	Ser	Asp	Pro	Ser	Leu	Thr	1075	1080	1085
Asn	Pro	Pro	Ala	Thr	Ile	Gln	Thr	Asp	Gly	Phe	Val	Lys	Tyr	Gly	Lys	1090	1095	1100
Ser	Ser	Tyr	Ser	Leu	Met	Arg	Gln	Lys	Phe	Gln	Trp	His	Glu	Ala	Glu			

1105		1110		1115		1120
Thr Tyr Cys Lys	Leu His Asn Ser	Leu Ile Ala Ser	Ile Leu Asp Pro			
	1125	1130	1135			
Tyr Ser Asn Ala Phe	Ala Trp Leu Gln Met	Glu Thr Ser Asn	Glu Arg			
	1140	1145	1150			
Val Trp Ile Ala Leu	Asn Ser Asn Leu Thr	Asp Asn Gln Tyr	Thr Trp			
	1155	1160	1165			
Thr Asp Lys Trp Arg	Val Arg Tyr Thr	Asn Trp Ala Ala	Asp Glu Pro			
	1170	1175	1180			
Lys Leu Lys Ser Ala	Cys Val Tyr Leu Asp	Leu Asp Gly Tyr	Trp Lys			
1185	1190	1195	1200			
Thr Ala His Cys Asn	Glu Ser Phe Tyr Phe	Leu Cys Lys Arg	Ser Asp			
	1205	1210	1215			
Glu Ile Pro Ala Thr	Glu Pro Pro Gln	Leu Pro Gly Arg	Cys Pro Glu			
	1220	1225	1230			
Ser Asp His Thr Ala	Trp Glu Ile Pro	Phe His Gly His	Cys Tyr Tyr			
	1235	1240	1245			
Ile Glu Ser Ser Tyr	Thr Arg Asn Trp	Gly Gln Ala Ser	Leu Glu Cys			
	1250	1255	1260			
Leu Arg Met Gly Ser	Ser Ser Leu Val Ser	Ile Glu Ser Ala	Ala Glu Ser			
1265	1270	1275	1280			
Ser Phe Leu Ser Tyr	Arg Val Glu Pro	Leu Lys Ser Lys	Thr Asn Phe			
	1285	1290	1295			
Trp Ile Gly Leu Phe	Arg Asn Val Glu	Gly Thr Trp Leu	Trp Ile Asn			
	1300	1305	1310			
Asn Ser Pro Val Ser	Phe Val Asn Trp	Asn Thr Gly Asp	Pro Ser Gly			
	1315	1320	1325			
Glu Arg Asn Asp Cys	Val Ala Leu His	Ala Ser Ser Gly	Phe Trp Ser			
	1330	1335	1340			
Asn Ile His Cys Ser	Ser Tyr Lys Gly Tyr	Ile Cys Lys Arg	Pro Lys			
1345	1350	1355	1360			
Ile Ile Asp Ala Lys	Pro Thr His Glu	Leu Leu Thr Thr	Lys Ala Asp			
	1365	1370	1375			
Thr Arg Lys Met Asp	Pro Ser Lys Pro	Ser Ser Asn Val	Ala Gly Val			
	1380	1385	1390			
Val Ile Ile Val Ile	Leu Leu Ile Leu	Thr Gly Ala Gly	Leu Ala Ala			
	1395	1400	1405			
Tyr Phe Phe Tyr Lys	Lys Arg Arg Val	His Leu Pro Gln	Glu Gly Ala			
	1410	1415	1420			
Phe Glu Asn Thr Leu	Tyr Phe Asn Ser	Gln Ser Ser Pro	Gly Thr Ser			
1425	1430	1435	1440			
Asp Met Lys Asp Leu	Val Gly Asn Ile	Glu Gln Asn Glu	His Ser Val			
	1445	1450	1455			

Ile

<210> 6
 <211> 30
 <212> PRT
 <213> mus musculus

<220>
 <223> C terminal DEC-205

<400> 6
 Arg Ser His Ile Arg Trp Thr Gly Phe Ser Ser Val Arg Tyr Glu His

1		5		10		15
Gly	Thr	Asn	Glu	Asp	Glu	Val
					Met	Leu
						Pro
						Ser
						Phe
						His
						Asp
		20			25	
						30

<210> 7
 <211> 6
 <212> PRT
 <213> homo sapiens

<220>
 <221> VARIANT
 <222> 1, 2, 4, 5, 6
 <223> Xaa at position 1 is aromatic; Xaa at position 2
 and 4 are aliphatic; Xaa at position 5 and 6 are
 any of Asp, Asn, Glu, or Gln.

<400> 7
 Xaa Xaa Gly Xaa Xaa Xaa
 1 5

<210> 8
 <211> 4
 <212> PRT
 <213> homo sapiens

<220>
 <221> VARIANT
 <222> 2, 4
 <223> Xaa at position 4 is aliphatic; Xaa at position 2
 is any of Asp, Asn, Glu, or Gln.

<400> 8
 Glu Xaa Cys Xaa
 1

<210> 9
 <211> 4
 <212> PRT
 <213> homo sapiens

<220>
 <221> VARIANT
 <222> 1, 2, 4
 <223> Xaa at position 1 is aromatic; Xaa at position 2
 and 4 are aliphatic.

<400> 9
 Xaa Xaa Gly Xaa
 1

<210> 10
 <211> 4
 <212> PRT

<213> homo sapiens

<220>

<221> VARIANT

<222> 1, 3, 4

<223> Xaa at position 1 is Glu or Gln; Xaa at position 3 and 4 are Asp or Asn.

<400> 10

Xaa Pro Xaa Xaa

1

<210> 11

<211> 5

<212> PRT

<213> homo sapiens

<220>

<221> VARIANT

<222> 1, 2, 4, 5

<223> Xaa at position 1 is aromatic; Xaa at position 2 and 4 are aliphatic; Xaa at position 5 is any of Asp, Asn, Glu, or Gln.

<400> 11

Xaa Xaa Gly Xaa Xaa

1

5

<210> 12

<211> 5

<212> PRT

<213> homo sapiens

<220>

<221> VARIANT

<222> 2, 4, 5

<223> Xaa at position 5 is aliphatic or aromatic; Xaa at position 4 is aliphatic; Xaa at position 2 is any of Asp, Asn, Glu, or Gln.

<400> 12

Glu Xaa Cys Xaa Xaa

1

5

<210> 13

<211> 19

<212> PRT

<213> Homo sapiens

<400> 13

Ser Glu Ser Ser Gly Asn Asp Pro Phe Thr Ile Val His Glu Asn Thr

1

5

10

15

Gly Lys Cys